

Fig. 1

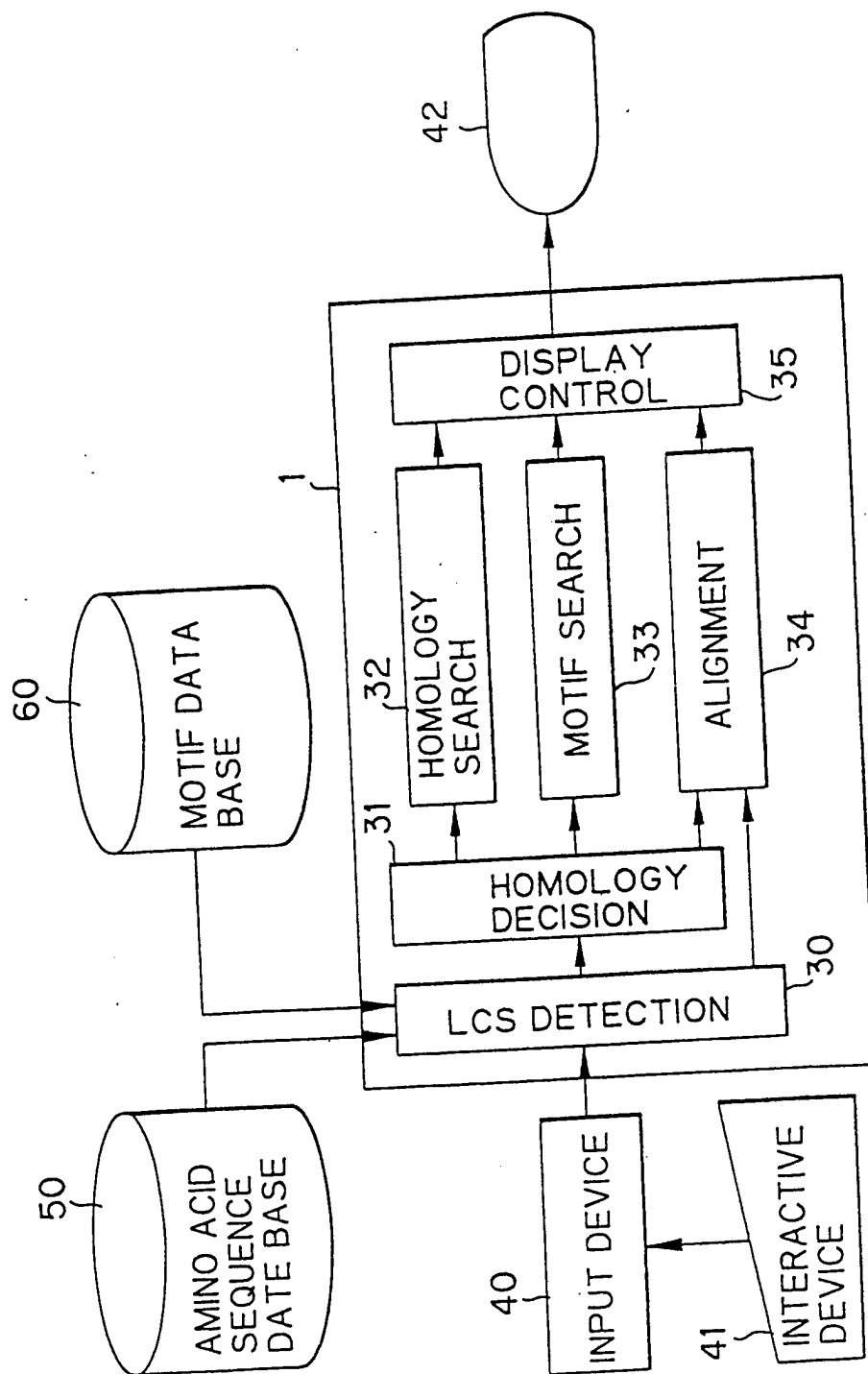


Fig. 2

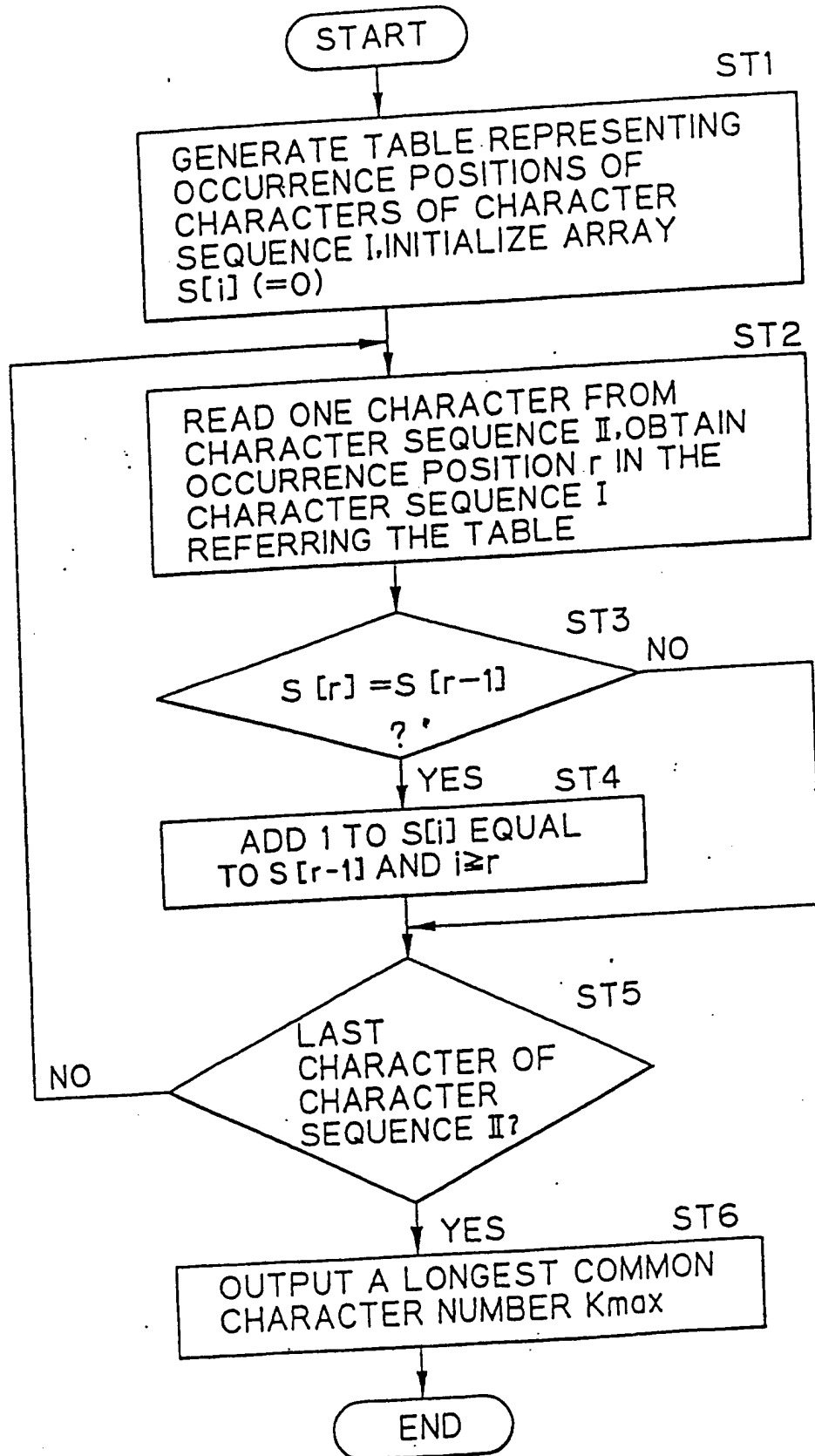


Fig. 3

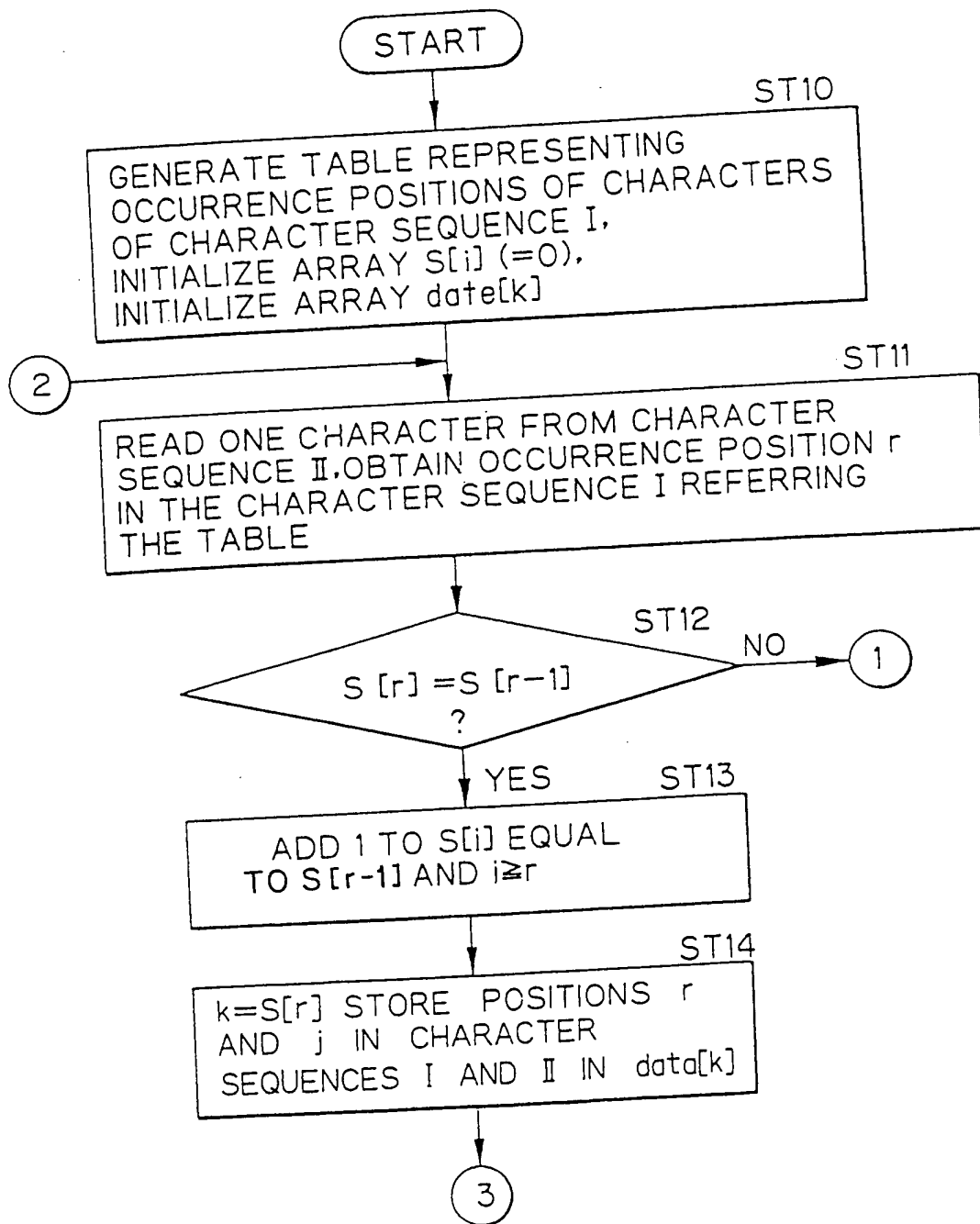


Fig. 4

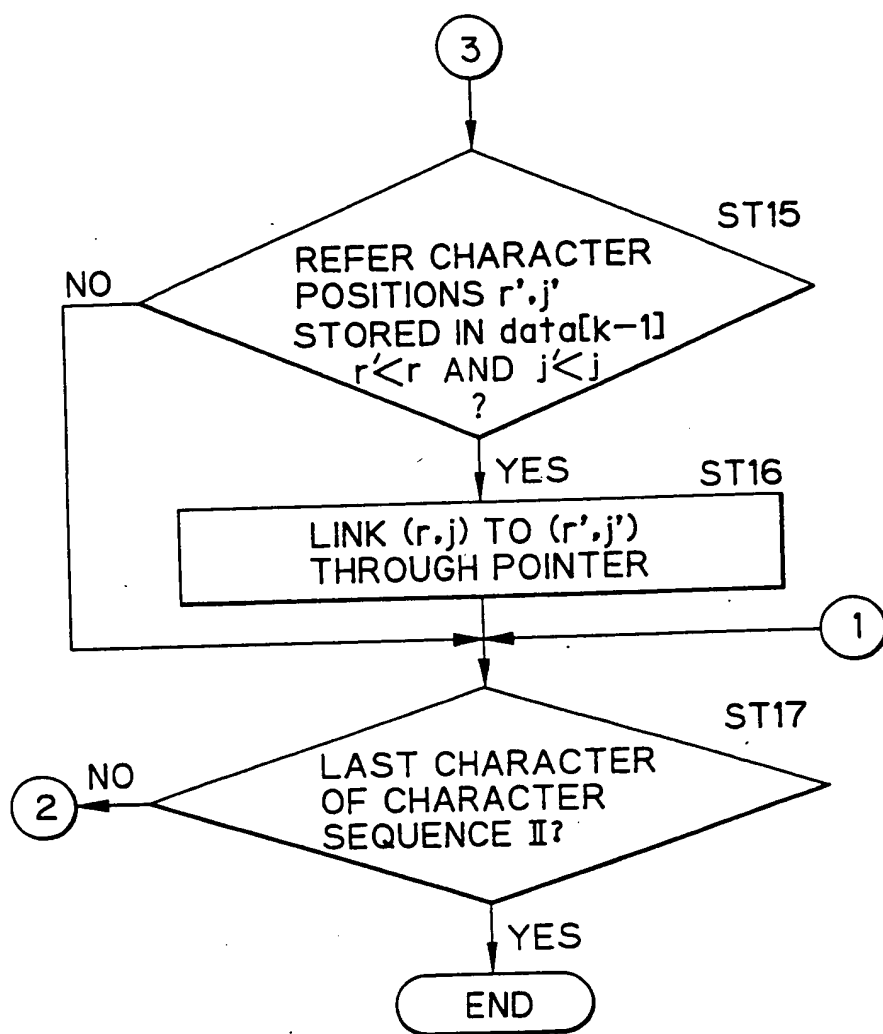


Fig. 5

CHARACTER SEQUENCE I="ABCB DAB"

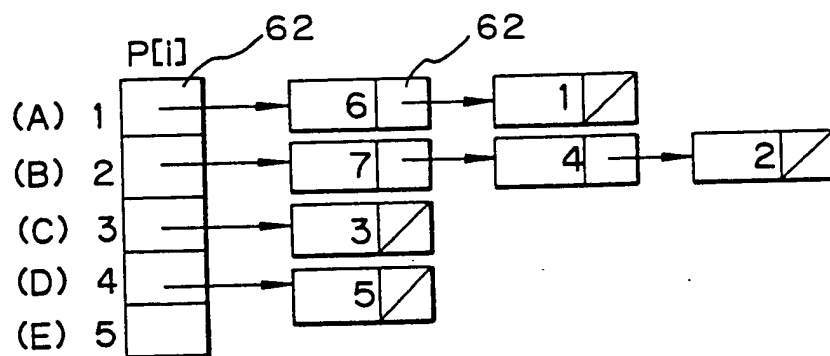


Fig. 6

CHARACTER SEQUENCE II = "BDCABA"

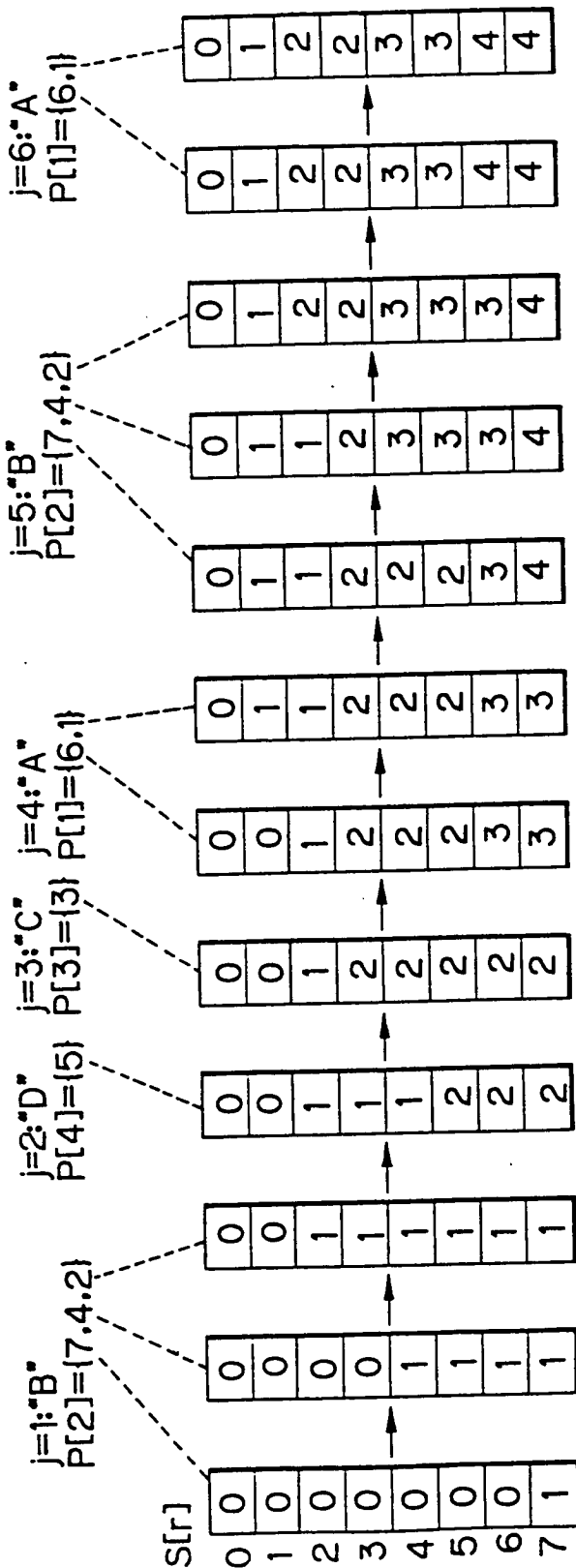


Fig. 8

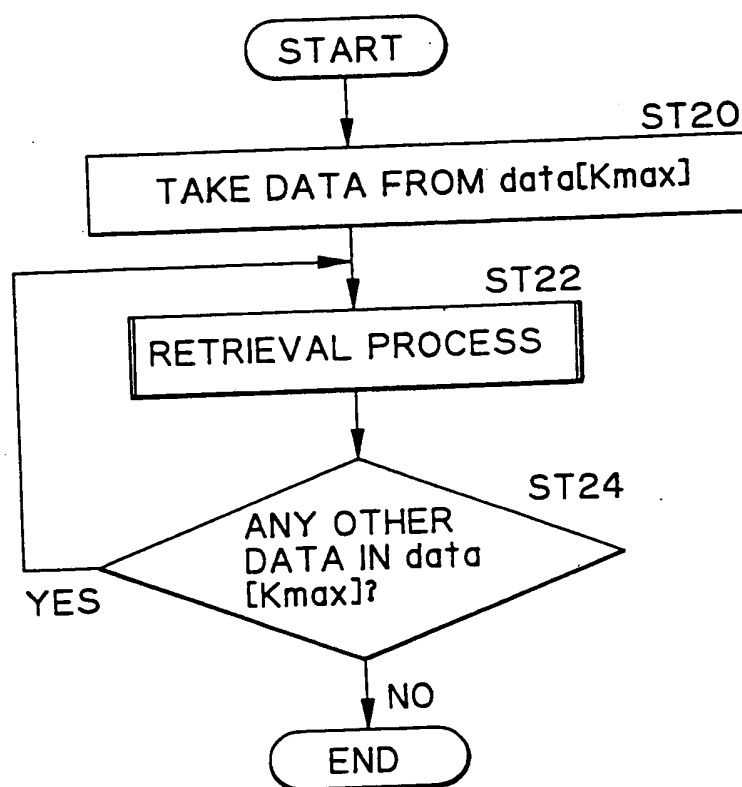
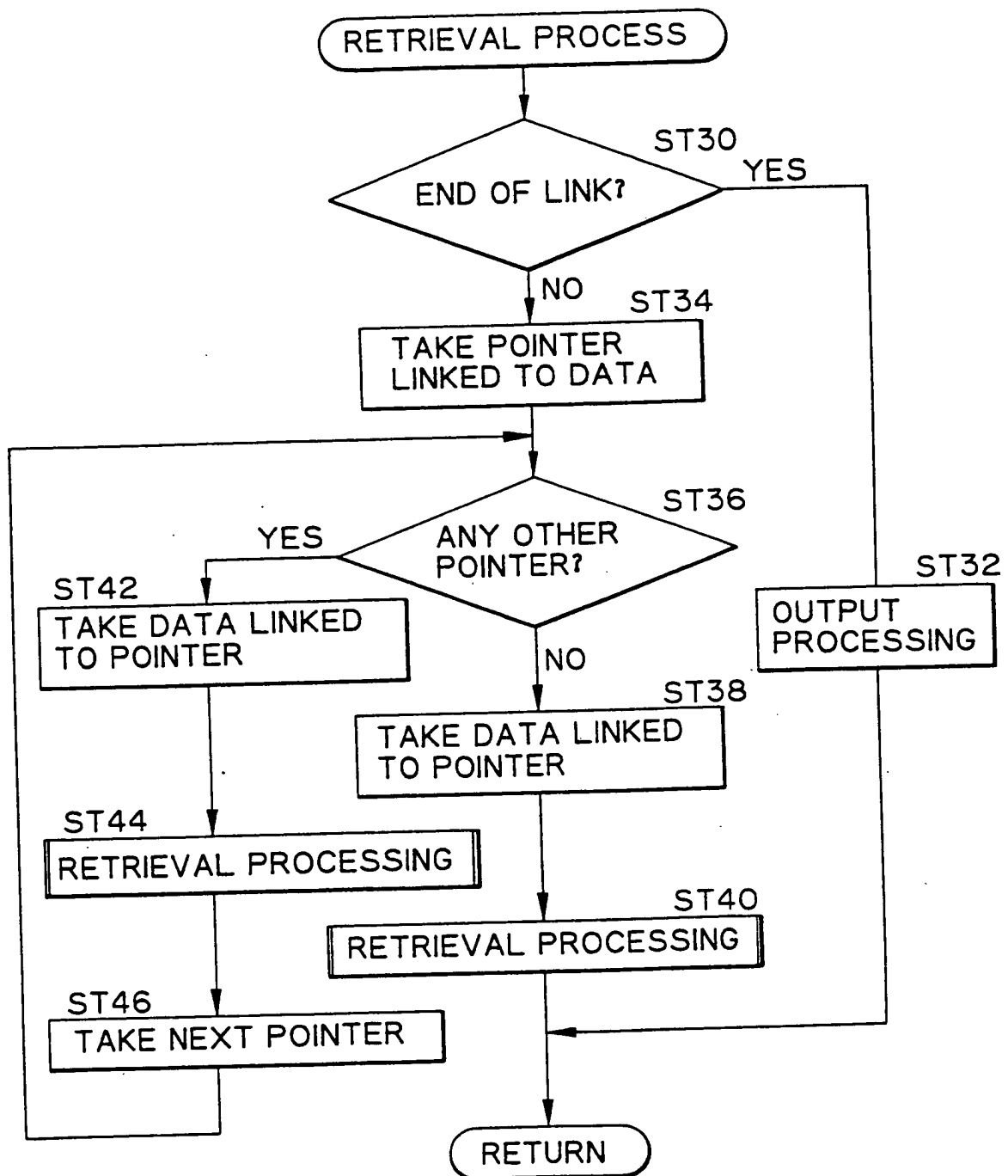


Fig. 9



LCS

homology : 47%

Fig. 12

human : GDVEK G K KIFIMKCSQCHTVEKGG KHKTPNHLHGLFGRK ...
bacterium : E GDAAAGEKVS KCLACHTFDQGGANKV GPNNP LFGVF...

Fig. 15

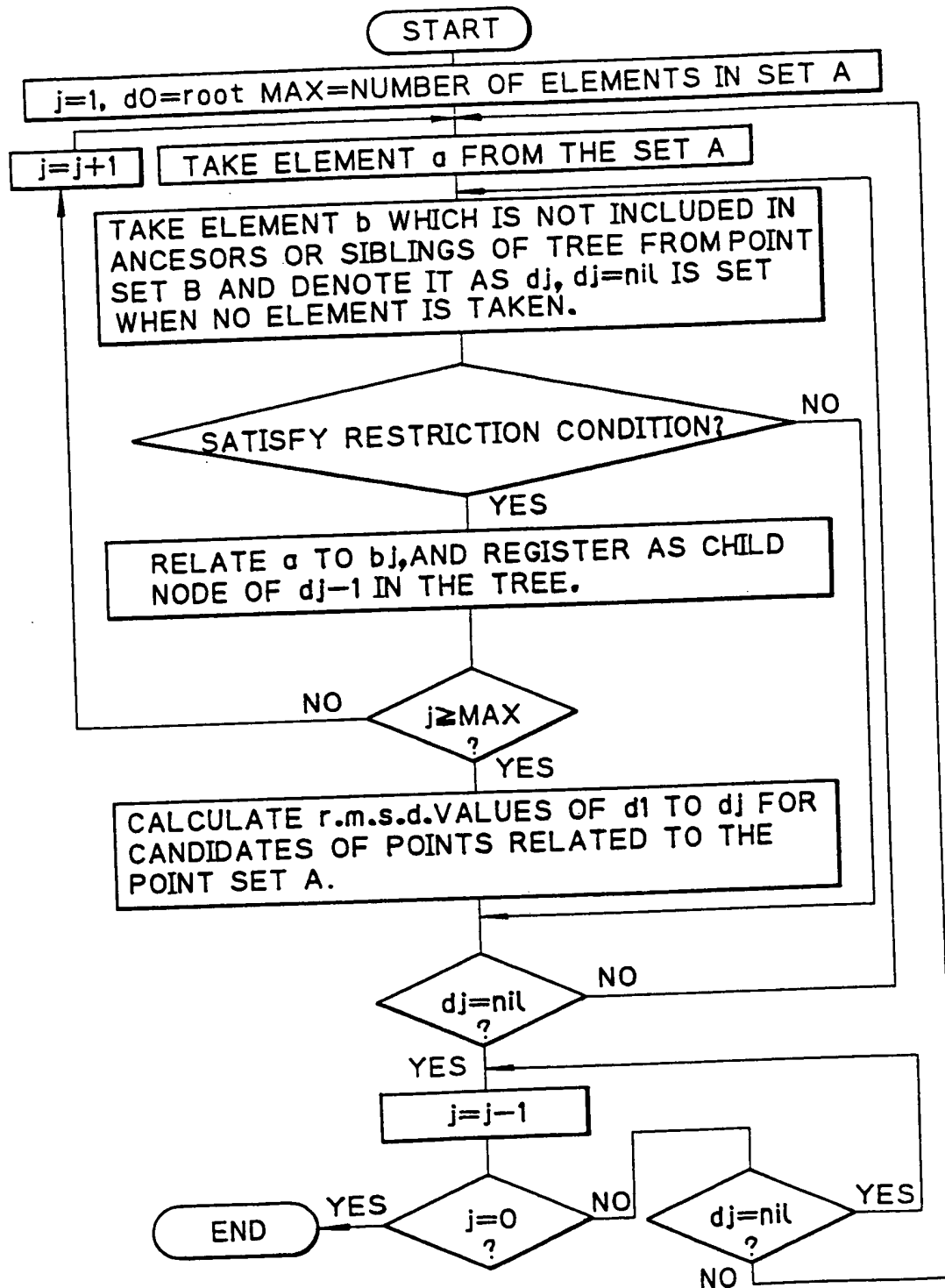


Fig. 16 A

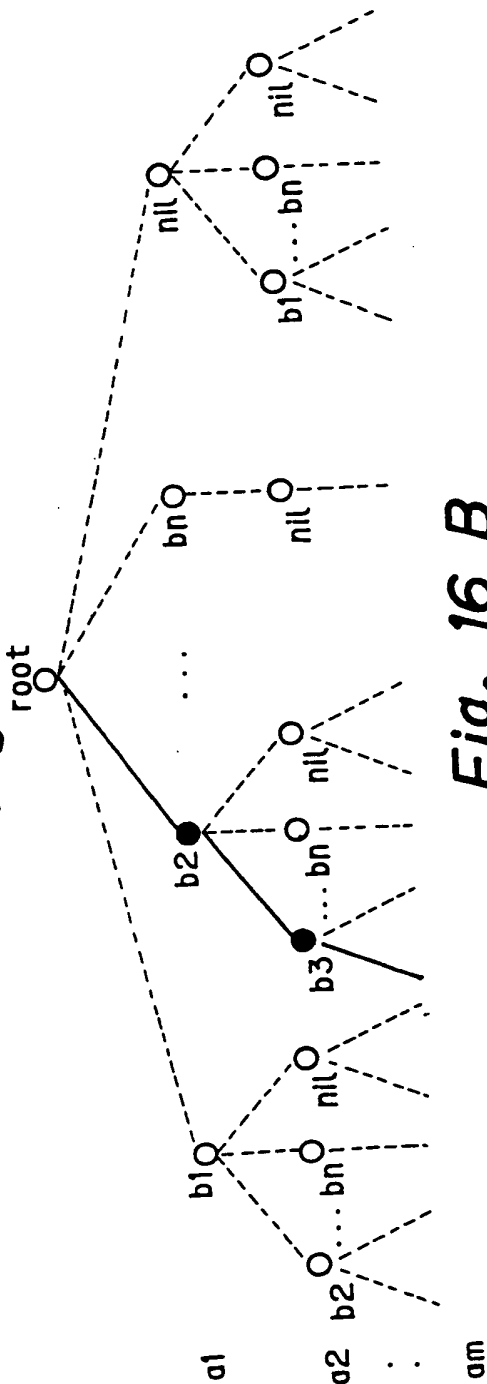


Fig. 16 B

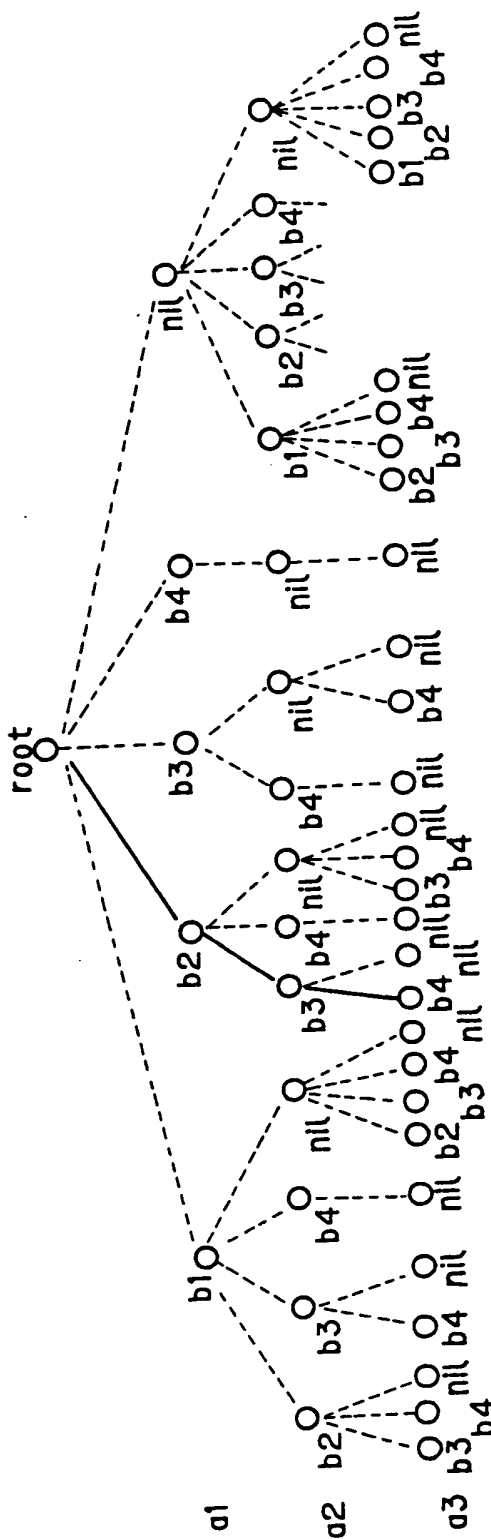


Fig. 17

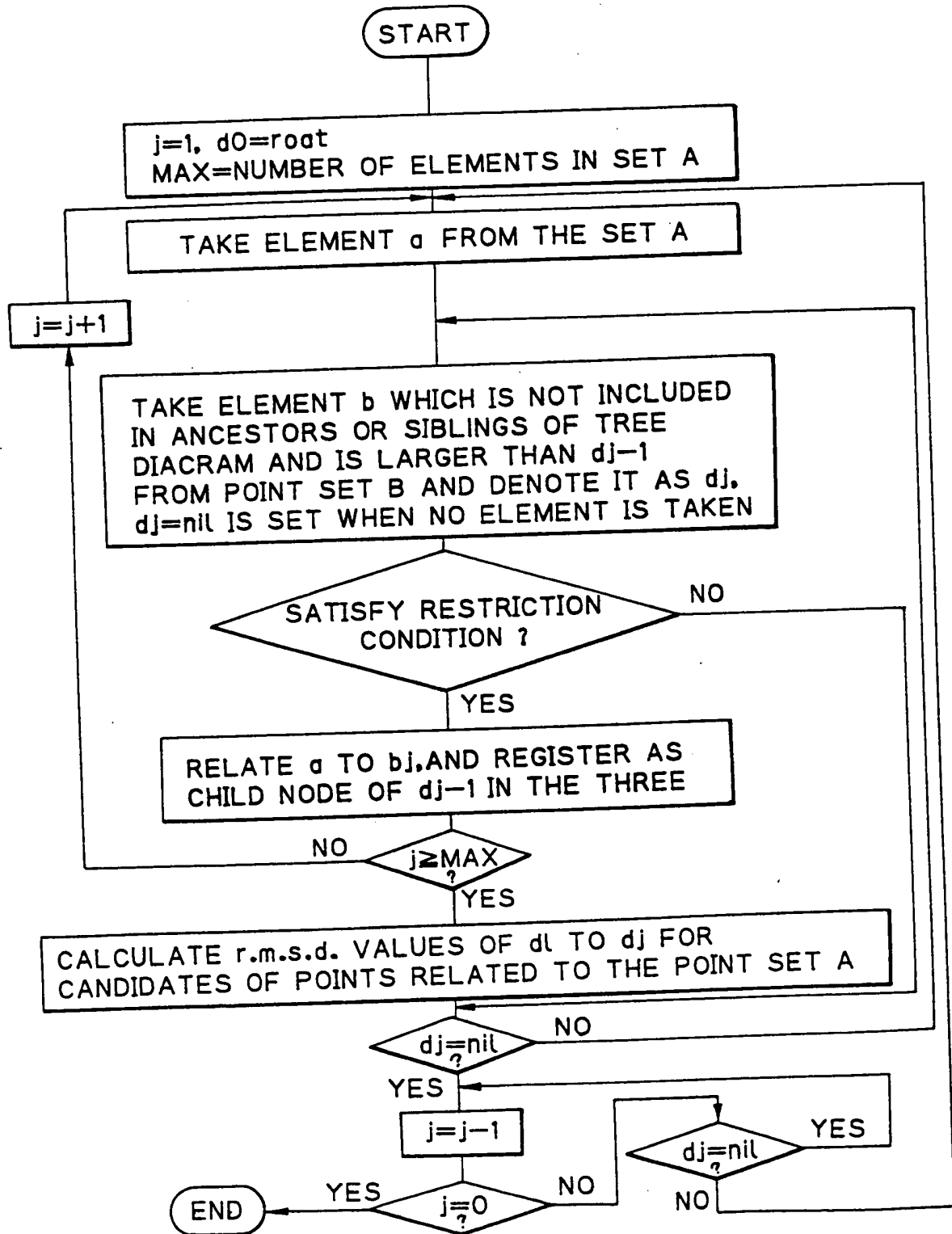


Fig. 19 A

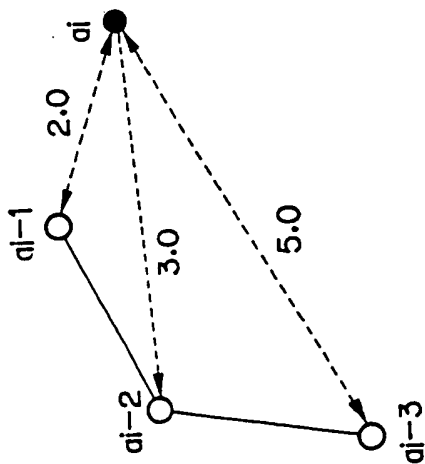


Fig. 19 B

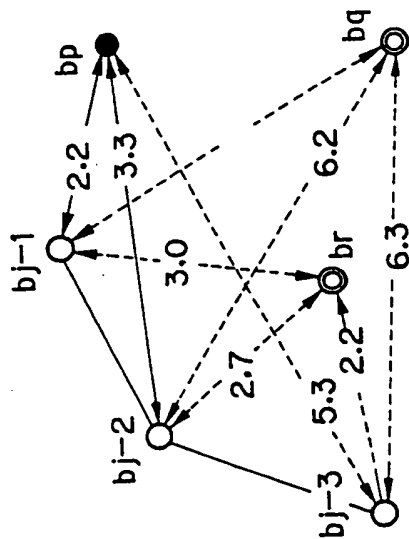


Fig. 20 A

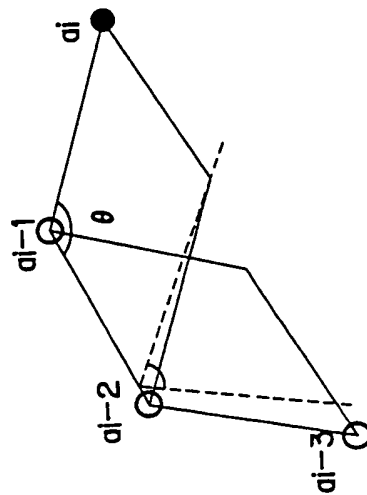


Fig. 20 B

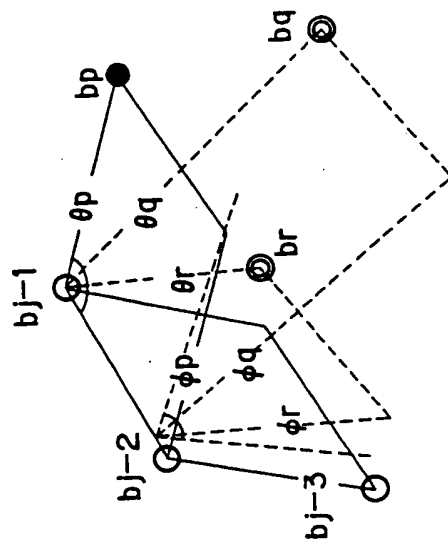


Fig. 21

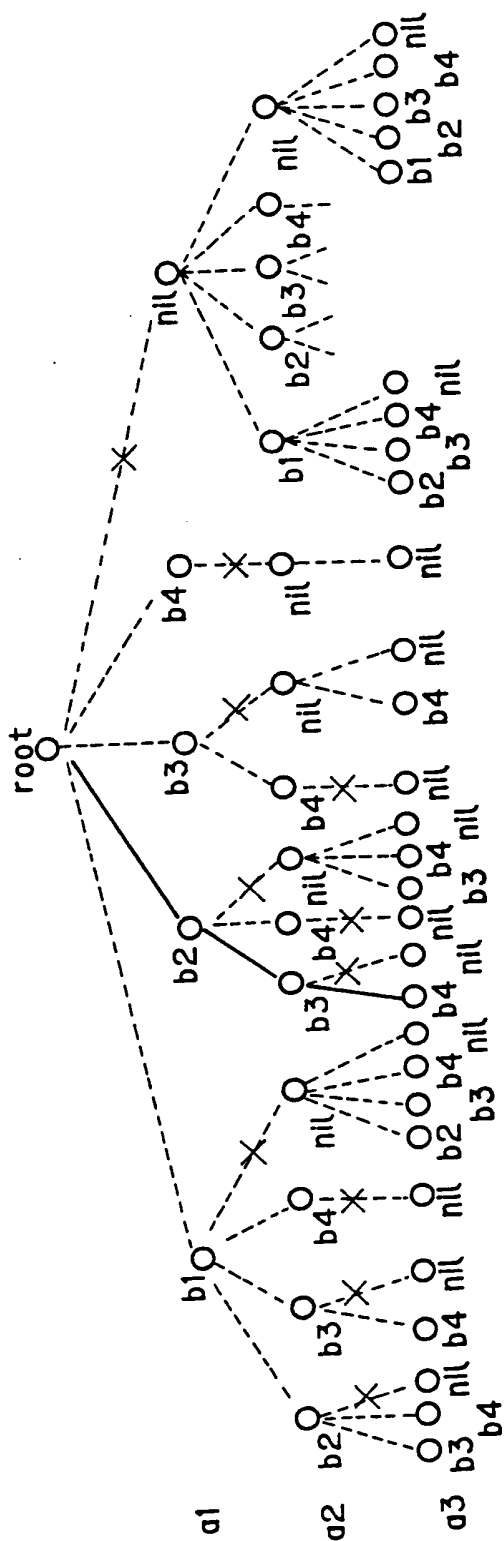
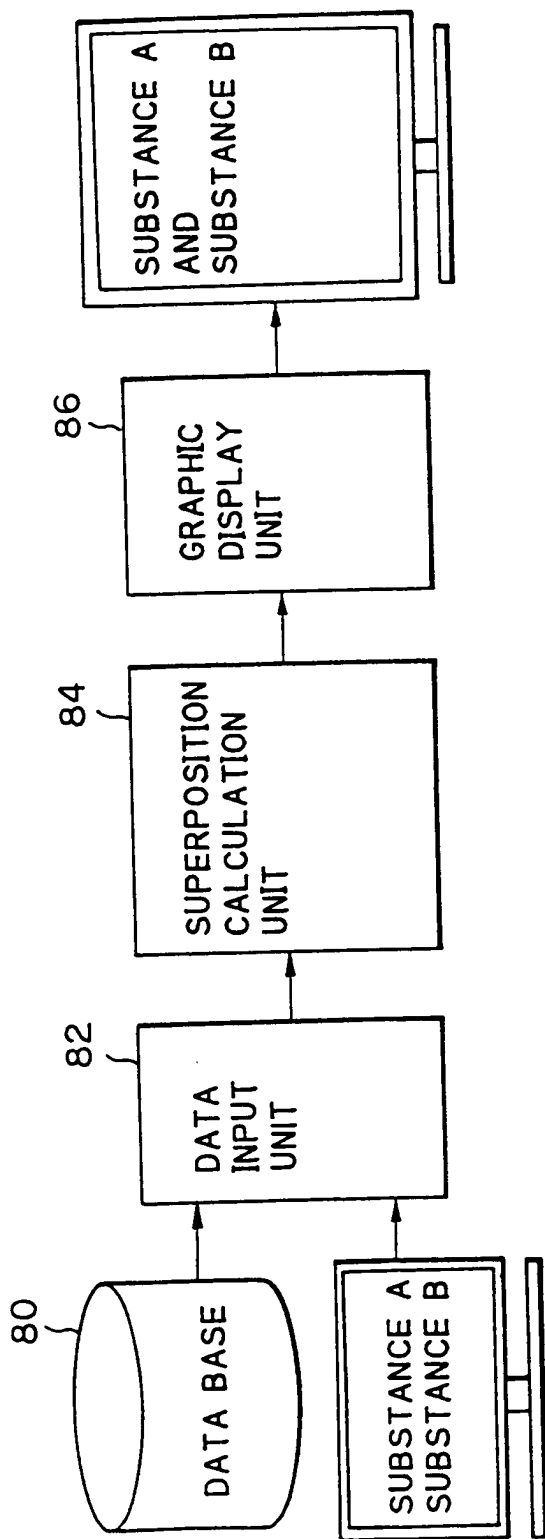


Fig. 22



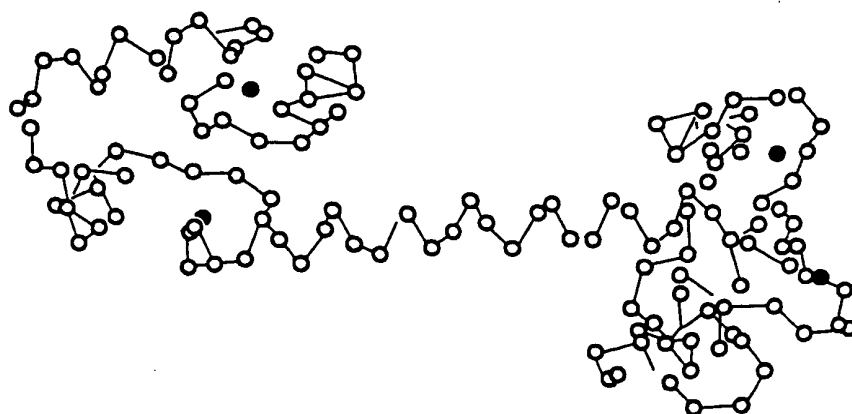
1	T E E Q I A E F K E	A F S L F D K D G D
21	G T I T T K E L G T	V M R S L G Q N P T
41	E A E L Q D M I N E	V D A D G N G T I D
61	F P E F L T M M A R	K M K D T D S E E E
81	I R E A F R V F D K	D G N G Y I S A A E
101	L R H V M T N L G E	K L T D E E V D E M
121	I R E A N I D G D G	Q V N Y E E F V Q M
141	M T A	

Fig. 23 B

1	A M D Q Q A E A R A	F L S E E M I A E F
21	K A A F D M F D A D	G G G D I S T K E L
41	G T V M R M L G Q N	P T K E E L D A I I
61	E E V D E D G S G T	I D F E E F L V M
81	V R Q M K E D A K G	K S E E E L A D C F
101	R I F D K N A D G F	I D I E E L G E I L
121	R A T G E H V T E E	D I E D L M K D S D
141	K N N D G R I D F D	E F L K M M E G V Q
161		

AMINO ACID SEQUENCE OF TROPONIN C
(EXCERPT FROM PDB)

CALMODULIN



TROPONIN C

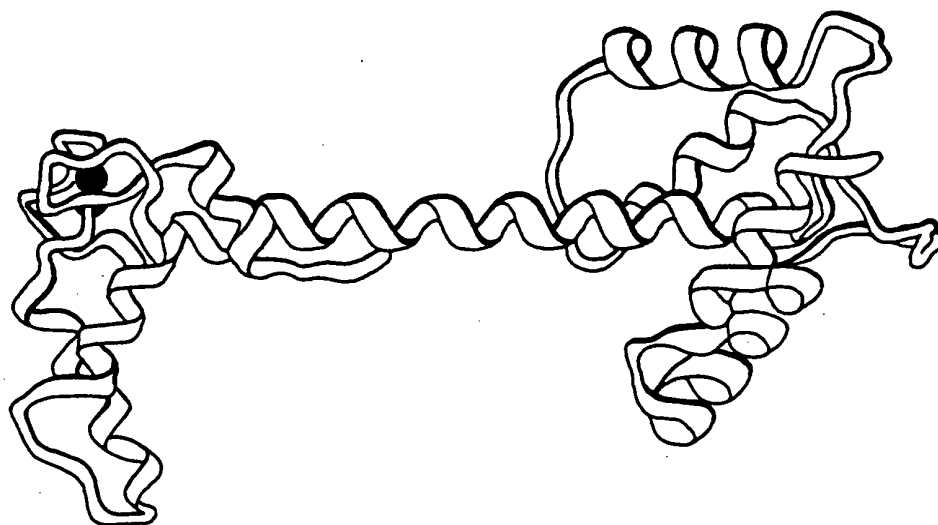


Fig. 25

Probe site = 81-108 in Calmodulin

	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	
L	A	D	C	F	R	I	F	D	K	N	A	D	G	F	< target	
I	R	E	A	F	R	V	F	D	K	D	G	N	G	Y	< probe	
I	I	I	I	I	E	E	L	G	E	I	L	R	A	T	< target	
I	S	A	A	A	E	E	L	R	H	V	M	T	N	L	< probe	

rmsd = 0.567034

Fig. 26

probe site = 81-108 and 117-143 in Calmodulin

96	97	98	99	100	101	102	103	104	105	106	107	108	109	110
L	A	D	C	F	R	I	F	D	K	N	A	D	G	F
>	<	<	<	<	<	<	<	<	<	<	<	<	<	< target >
I	R	E	A	F	R	V	F	D	K	D	G	N	G	Y
>	<	<	<	<	<	<	<	<	<	<	<	<	<	< probe >
111	112	113	114	115	116	117	118	119	120	121	122	123		
I	D	I	E	E	L	G	E	I	L	R	A	T		< target >
I	S	A	A	E	L	R	H	V	M	T	N	L		< probe >
132	133	134	135	136	137	138	139	140	141	142	143	144	145	
I	E	D	L	M	K	D	S	D	K	N	N	D	G	< target >
V	D	E	M	I	R	E	A	N	I	D	G	D	G	< probe >
146	147	148	149	150	151	152	153	154	155	156	157	158		
R	I	D	F	D	E	F	L	K	M	M	E	G		< target >
Q	V	N	Y	E	E	F	V	Q	M	M	T	A		< probe >

$$\text{rmsd} = 0.823665$$

Fig. 27

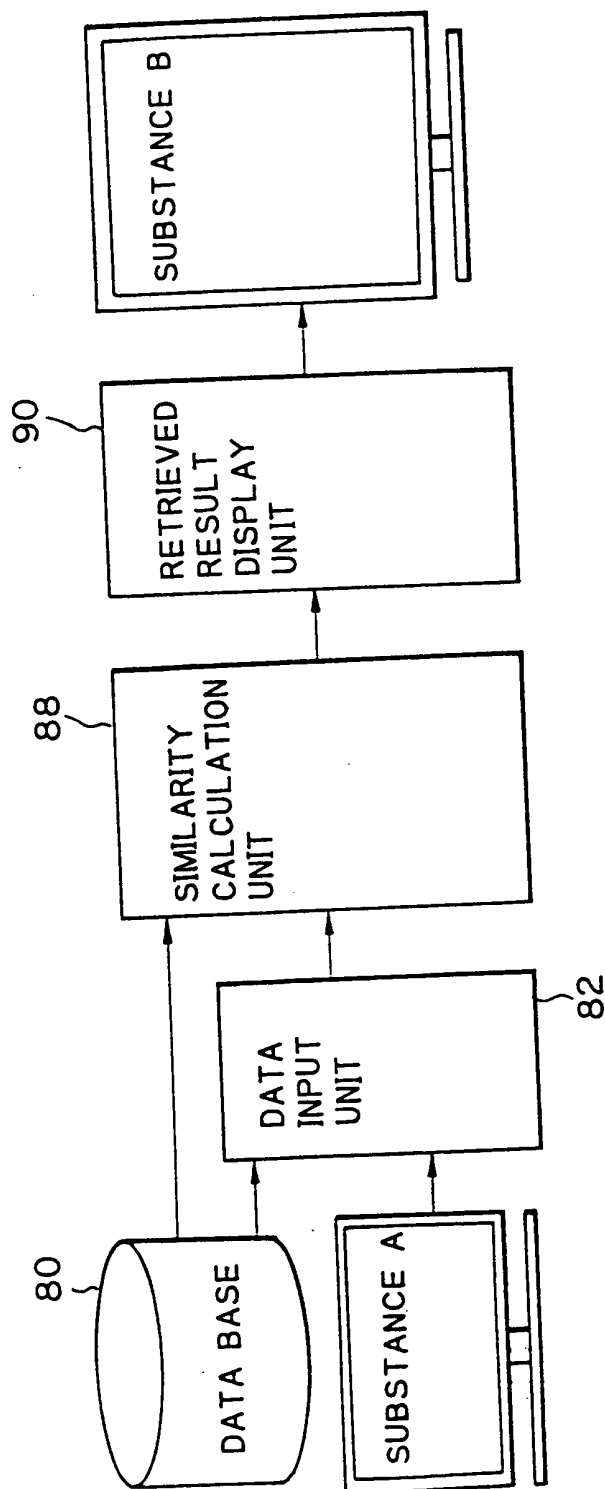


Fig. 28

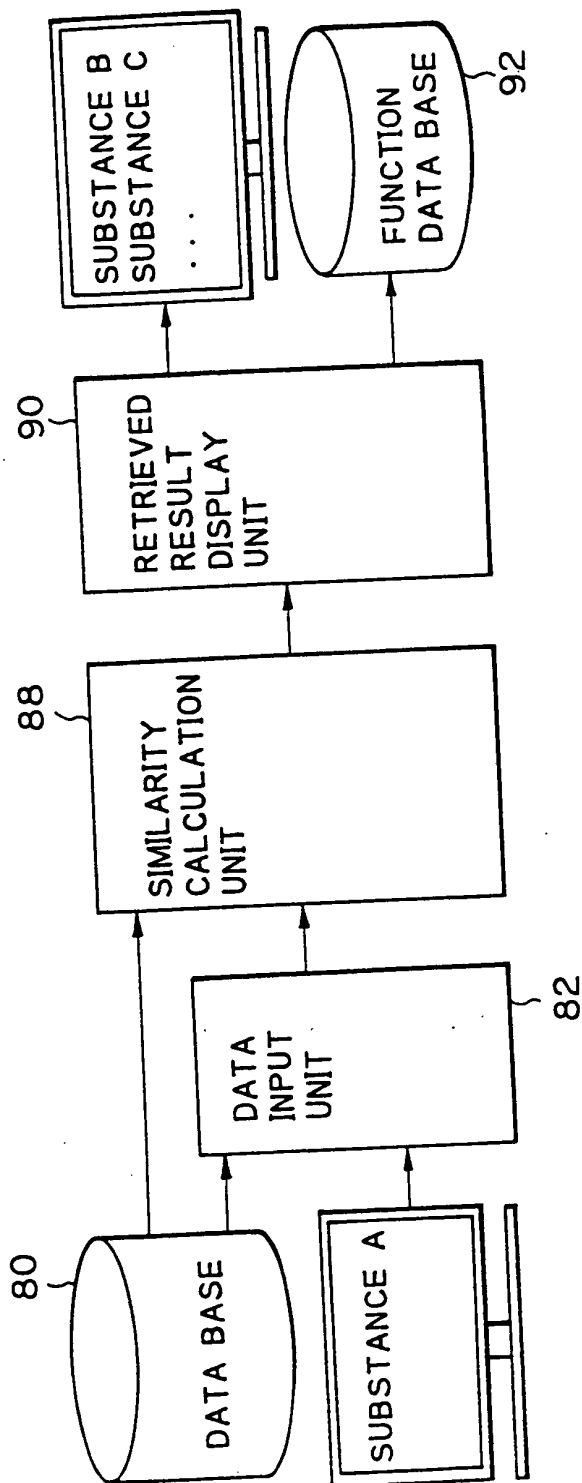


Fig. 29

===== ATP/GTP binding site =====

Probe = (elongation factor)

7 8 9 10 11 12 13 14
G H V D H G K T < probe >

8 9 10 11 12 13 14 15
G A P G S G K G < target >
G H V D H G K T < probe >
rmsd=0.648732 adenylate kinase

unit - A

. : . : .
10 11 12 13 14 15 16 17
G A G G V G K S < target >
G H V D H G K T < probe >
rmsd=0.421770 ras protein

Fig. 31

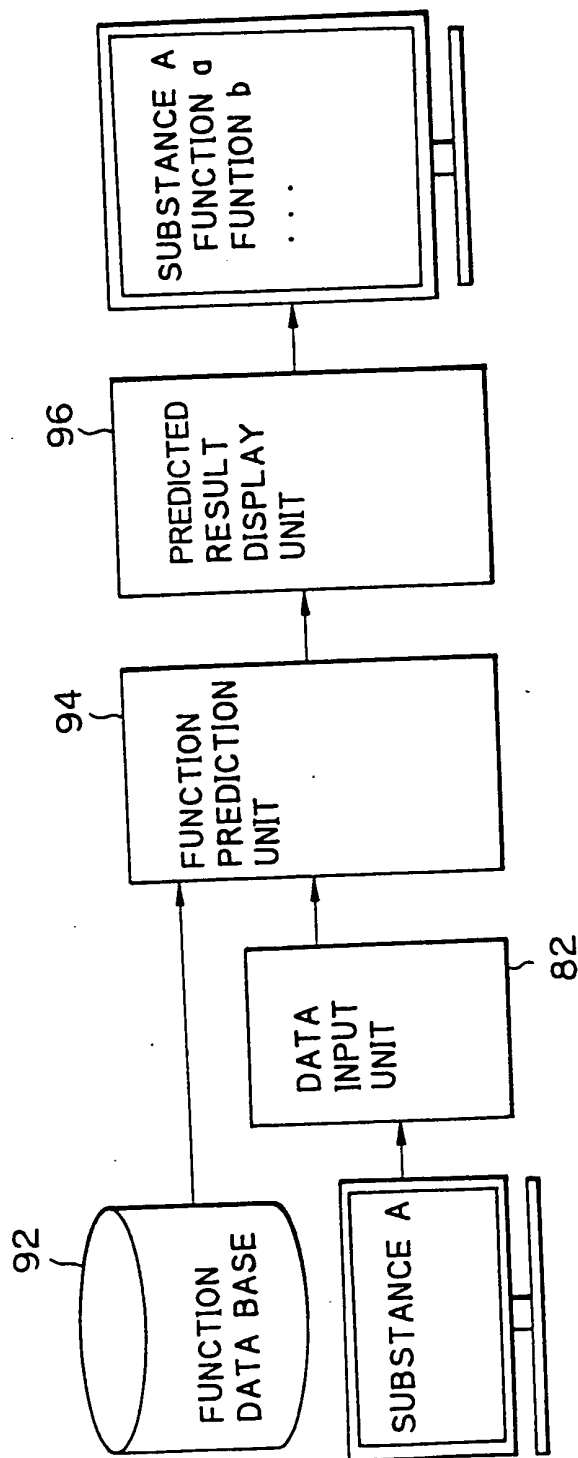


Fig. 32 A

Fig. 32 B

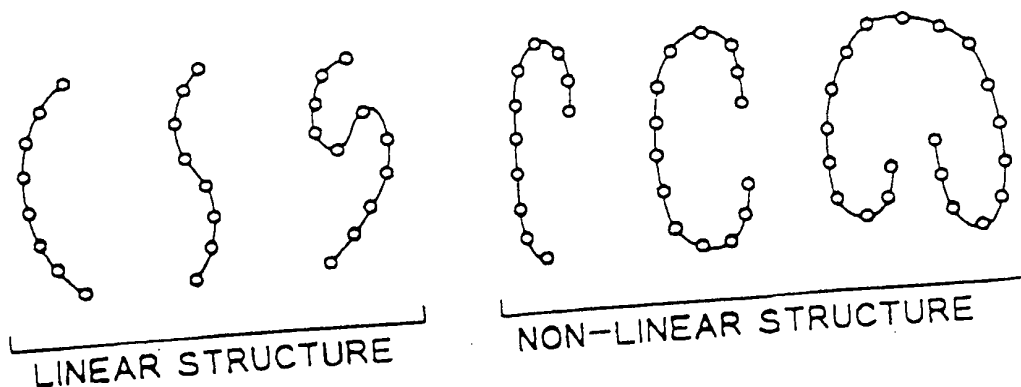
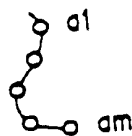
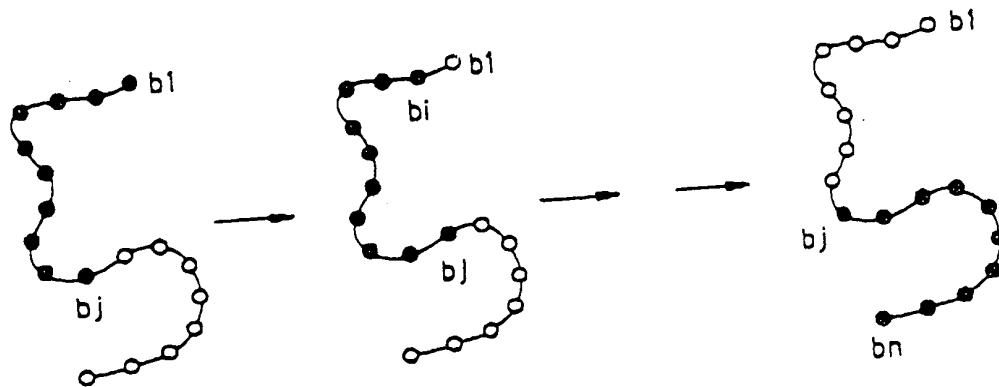


Fig. 33

WHEN $f(x)=2x$



$A=\{a_1, \dots, a_m\}$



$B=\{b_1, \dots, b_i, \dots, b_j, \dots, b_n\}$

Fig. 34

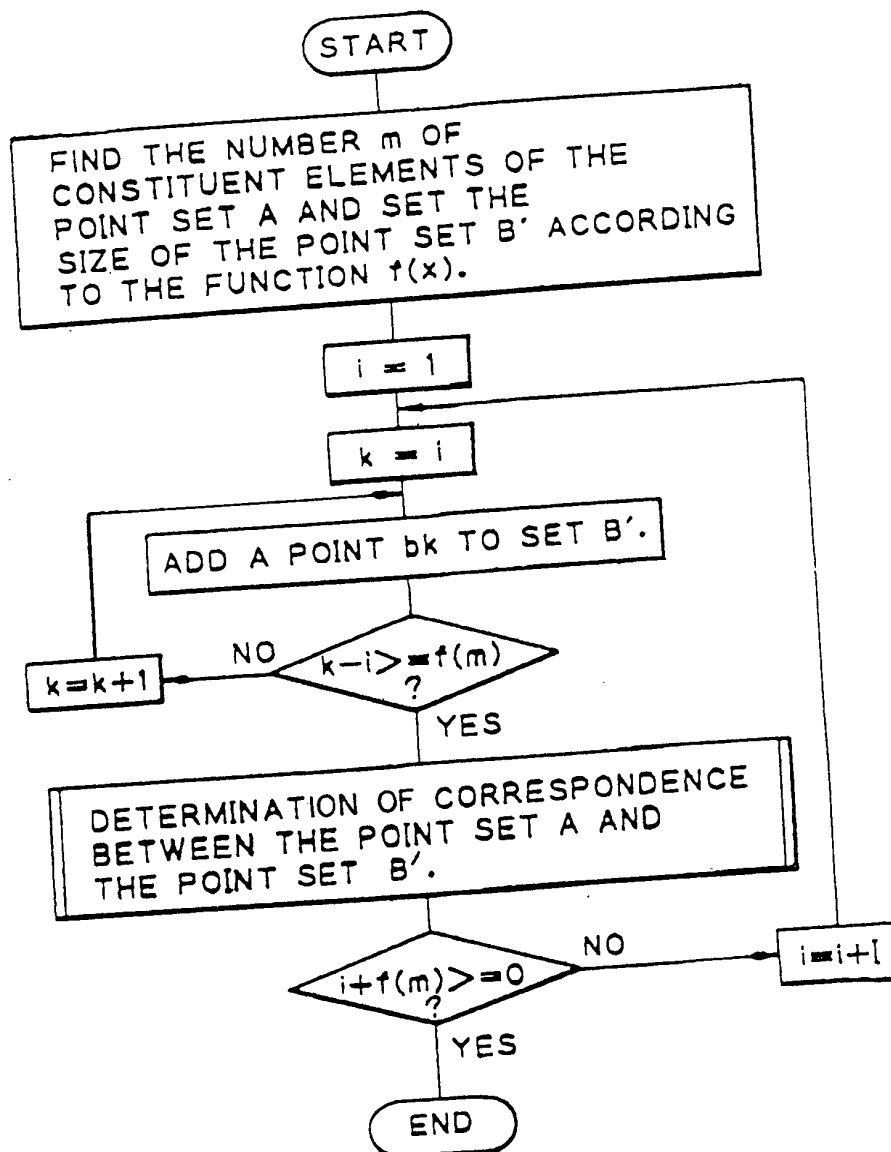
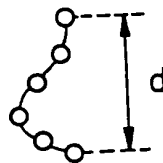
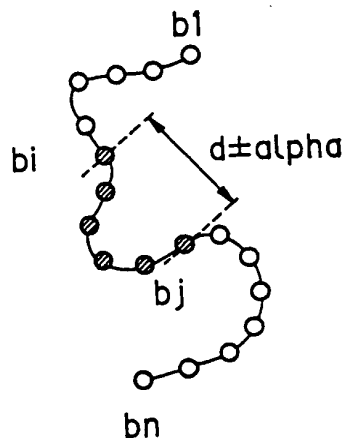


Fig. 35 A



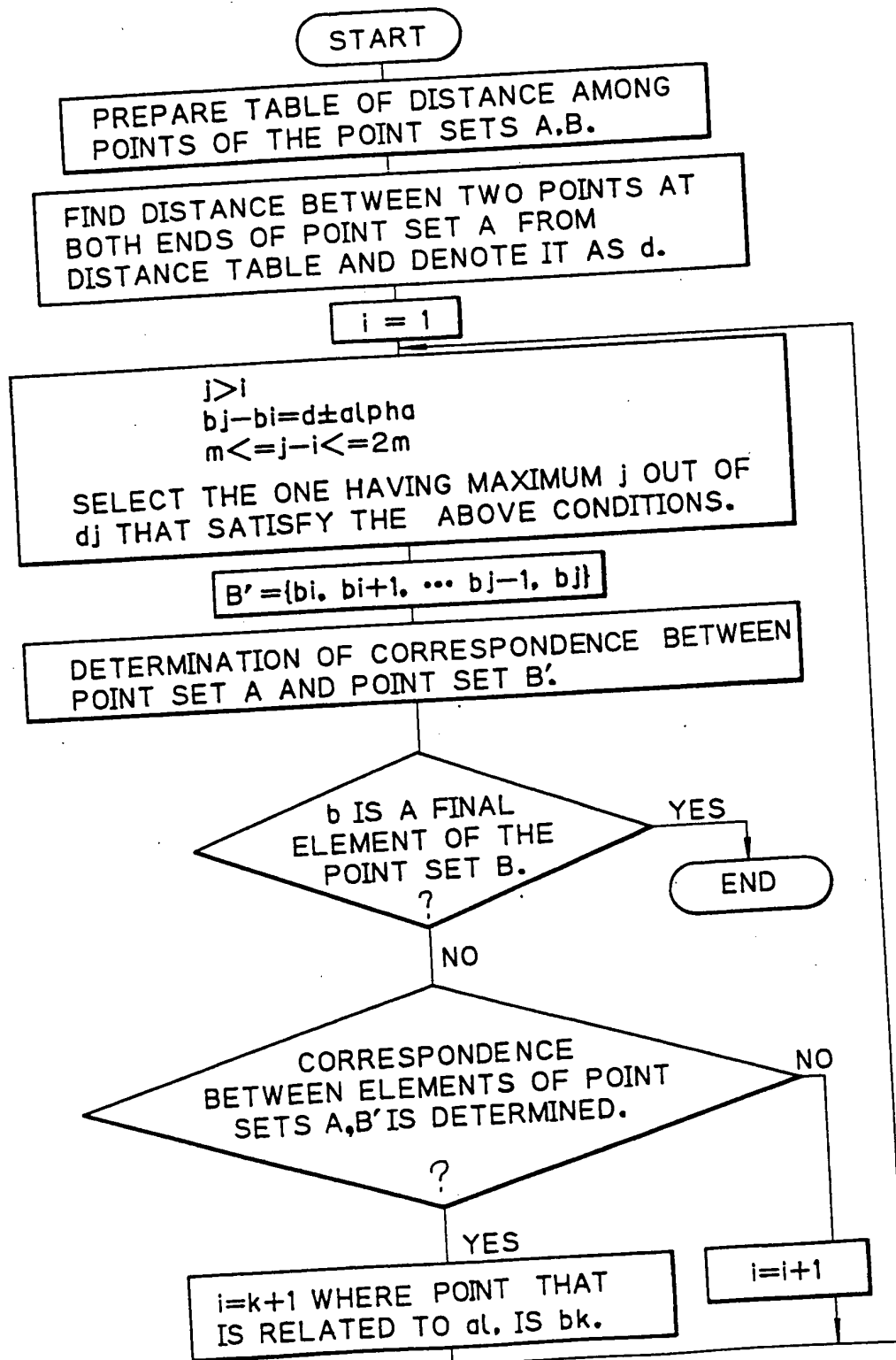
$$A = \{a_1, a_2, \dots, a_m\}$$

Fig. 35 B



$$B = \{b_1, \dots, b_i, \dots, b_j, \dots, b_n\}$$

Fig. 36



FOU-20-12001660

Fig. 37

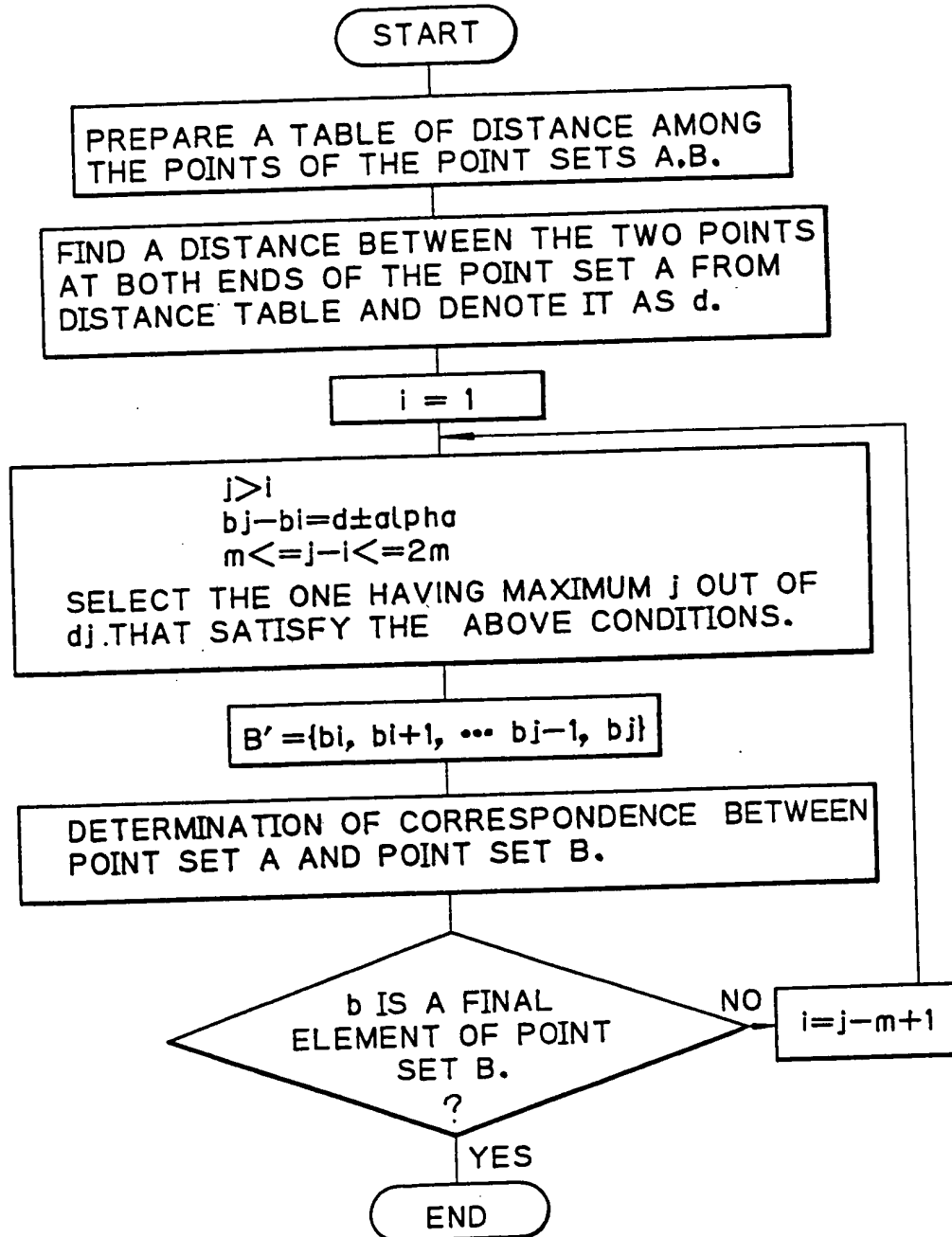


Fig. 38 A

1	I	V	G	G	Y	T	C	C	A	N	T	V	P	Y	Q	V	S	L	N	S
21	G	Y	H	F	C	G	G	S	L	I	N	S	Q	W	V	V	S	A	A	H
41	C	Y	K	S	G	I	Q	V	R	L	G	E	D	N	I	N	V	V	E	G
61	N	E	Q	F	I	S	A	S	K	S	I	V	H	P	S	Y	N	S	N	T
81	L	N	N	D	I	M	L	I	K	L	K	S	A	A	S	L	N	S	R	V
101	A	S	I	S	L	P	T	S	C	A	S	A	G	T	Q	C	L	I	S	G
121	W	G	N	T	K	S	S	G	T	S	Y	P	D	V	L	K	C	L	K	A
141	P	I	L	S	D	S	S	C	K	S	A	Y	P	G	Q	I	T	S	N	M
161	F	C	A	G	Y	L	E	G	G	K	D	S	C	Q	G	D	S	G	G	P
181	V	V	C	S	G	K	L	Q	G	I	V	S	W	G	S	G	C	A	Q	K
201	N	K	P	G	V	Y	T	K	V	C	N	Y	V	S	W	I	K	Q	T	I
221	A	S	N																	

AMINO ACID SEQUENCE OF TRYPSIN (EXCERPT FROM PDB)

Fig. 38 B

1	V	V	G	G	T	E	A	Q	R	N	S	W	P	S	Q	I	S	L	Q	Y
21	R	S	G	S	S	W	A	H	T	C	G	G	T	L	I	R	Q	N	W	V
41	M	T	A	A	H	C	V	D	R	E	L	T	F	R	V	V	V	G	E	H
61	N	L	N	Q	N	N	G	T	E	Q	Y	V	G	V	Q	K	I	V	V	
81	P	Y	W	N	T	D	D	V	A	A	G	Y	D	I	A	L	L	R	L	A
101	Q	S	V	T	L	N	S	Y	V	Q	L	G	V	L	P	R	A	G	T	I
121	L	A	N	S	P	C	Y	I	T	T	G	W	G	L	T	R	T	N	G	Q
141	L	A	Q	T	L	Q	Q	A	Y	L	P	T	V	D	Y	A	I	C	S	S
161	S	S	Y	W	G	S	T	V	K	N	S	M	V	C	A	G	G	D	G	V
181	R	S	G	C	Q	G	D	S	G	G	P	L	H	C	L	V	N	G	Q	Y
201	A	V	H	G	V	T	S	F	V	S	R	L	G	C	N	V	T	R	K	P
221	T	V	F	T	R	V	S	A	Y	I	S	W	I	N	N	V	I	A	S	N

AMINO ACID SEQUENCE OF ELASTASE (EXCERPT FROM PDB)

Fig. 39 A

Key site number 36 - 41 in Trypsin

41	42	43	44	45	46	
M	T	A	A	H	C	< target >
V	S	A	A	H	C	< probe >

d = 12.070038 [A]

r.m.s.d. = 0.061077 [A]

The number of atoms in a probe = 6

The number of atoms in PDB = 240

The number of combination = 1

Time = 1sec

RETRIEVED RESULTS OF HISTIDINE ACTIVE SITES

Fig. 39 B

Key site number 175 - 179 in Trypsin

186	187	188	189	190	
G	D	S	G	G	< target >
G	D	S	G	G	< probe >

d = 8.922721 [A]

r.m.s.d. = 0.092879 [A]

The number of atoms in a probe = 5

The number of atoms in PDB = 240

The number of combination = 1

Time = 1sec

RETRIEVED RESULTS OF SERINE ACTIVE SITES

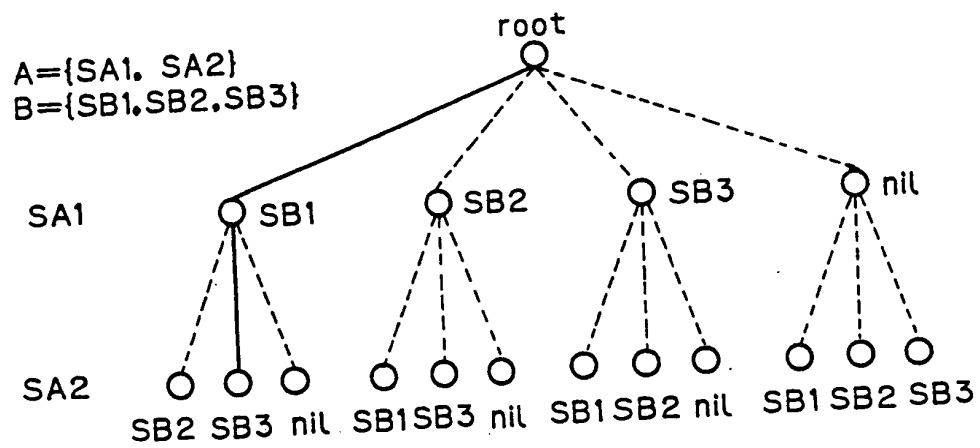
Fig. 40

Fig. 41

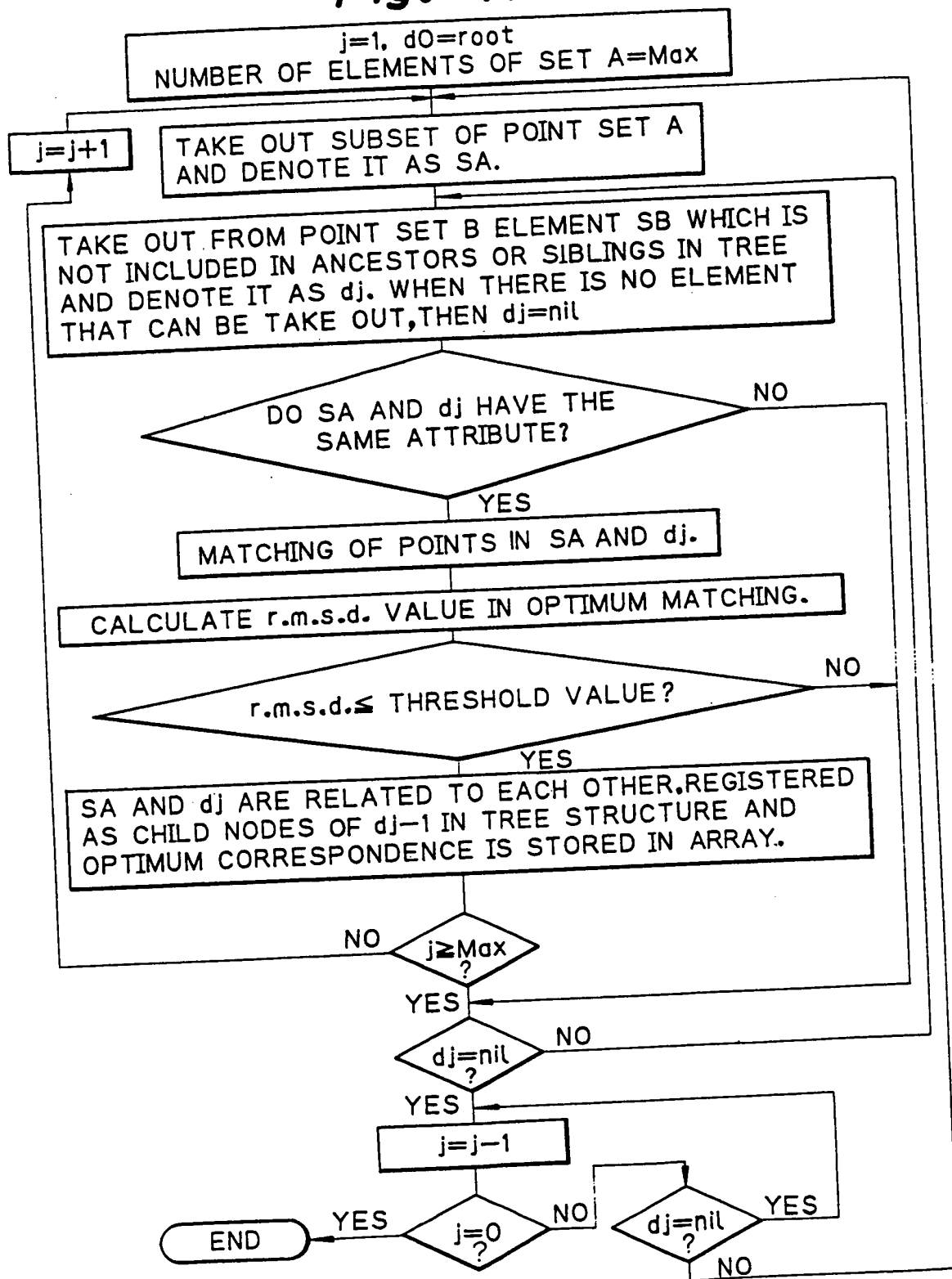


Fig. 42

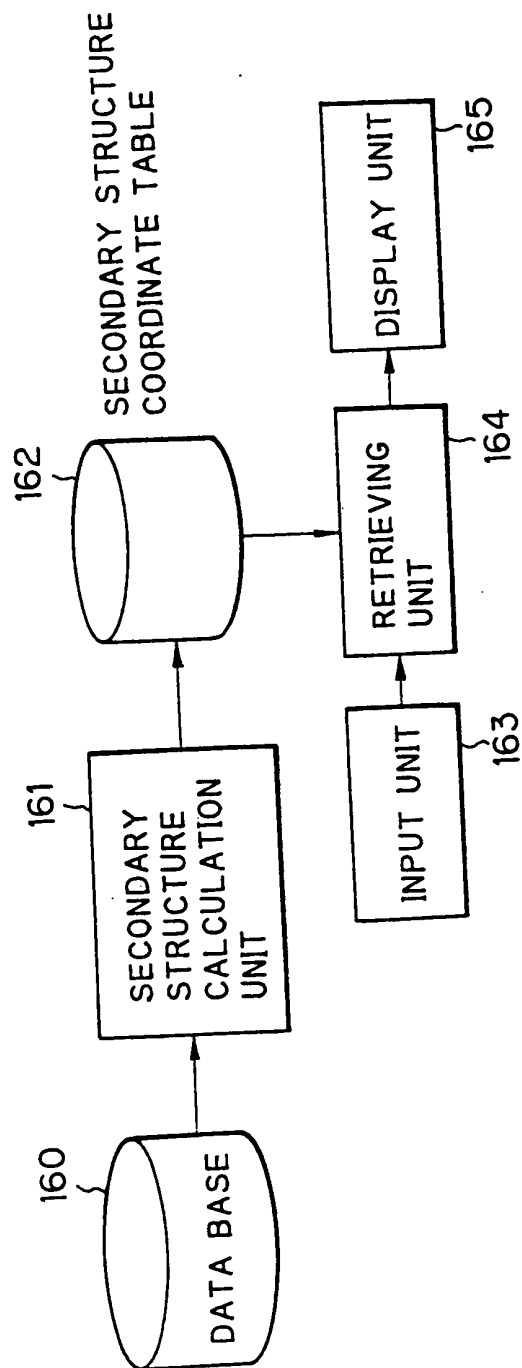
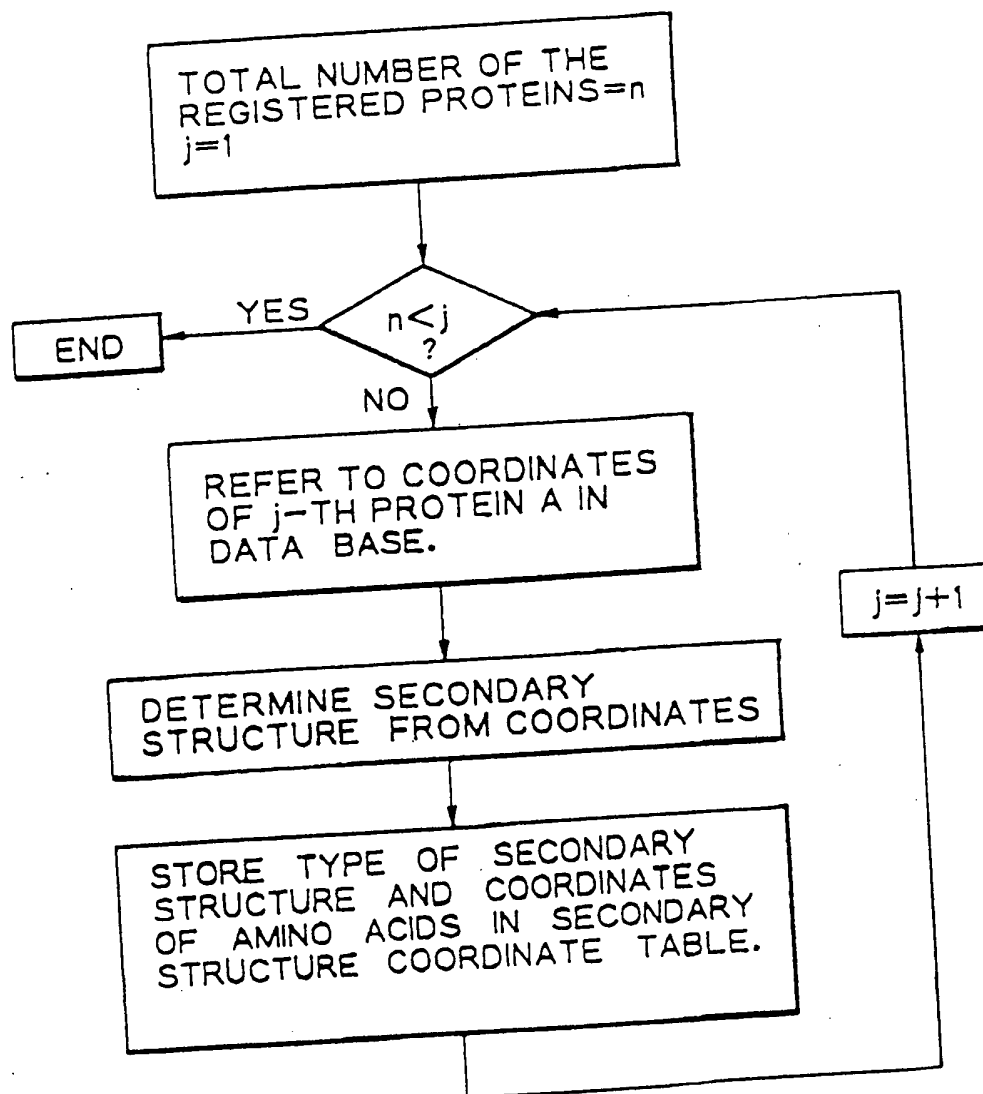


Fig. 43



00040074 02204

162

SUBSET	COORDINATES	TYPE
S1	{X1,X2,X3,X4,.....Xa}	α - HELIX
S2	{Xa+1,Xa+2,.....Xb}	α - HELIX
S3	{Xb+1,Xb+2,.....Xc}	β - SHEET
S4	{Xc+1,Xc+2,.....Xd}	β - SHEET
	⋮	⋮
Sn	{Xi+1,Xi+2,.....Xm}	3 - TURN

Fig. 45

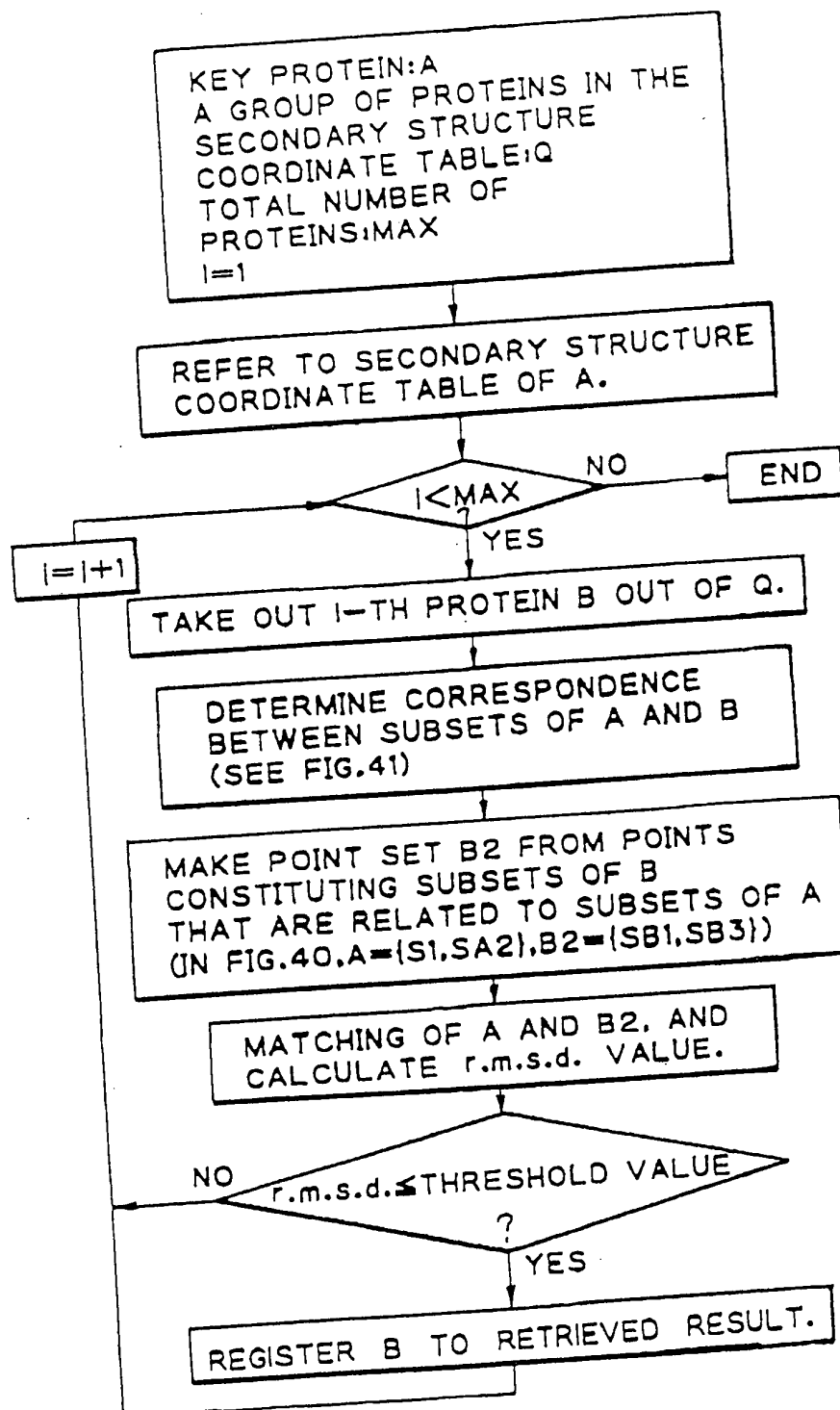
00040004 072304
00000000 00000000

Fig. 46

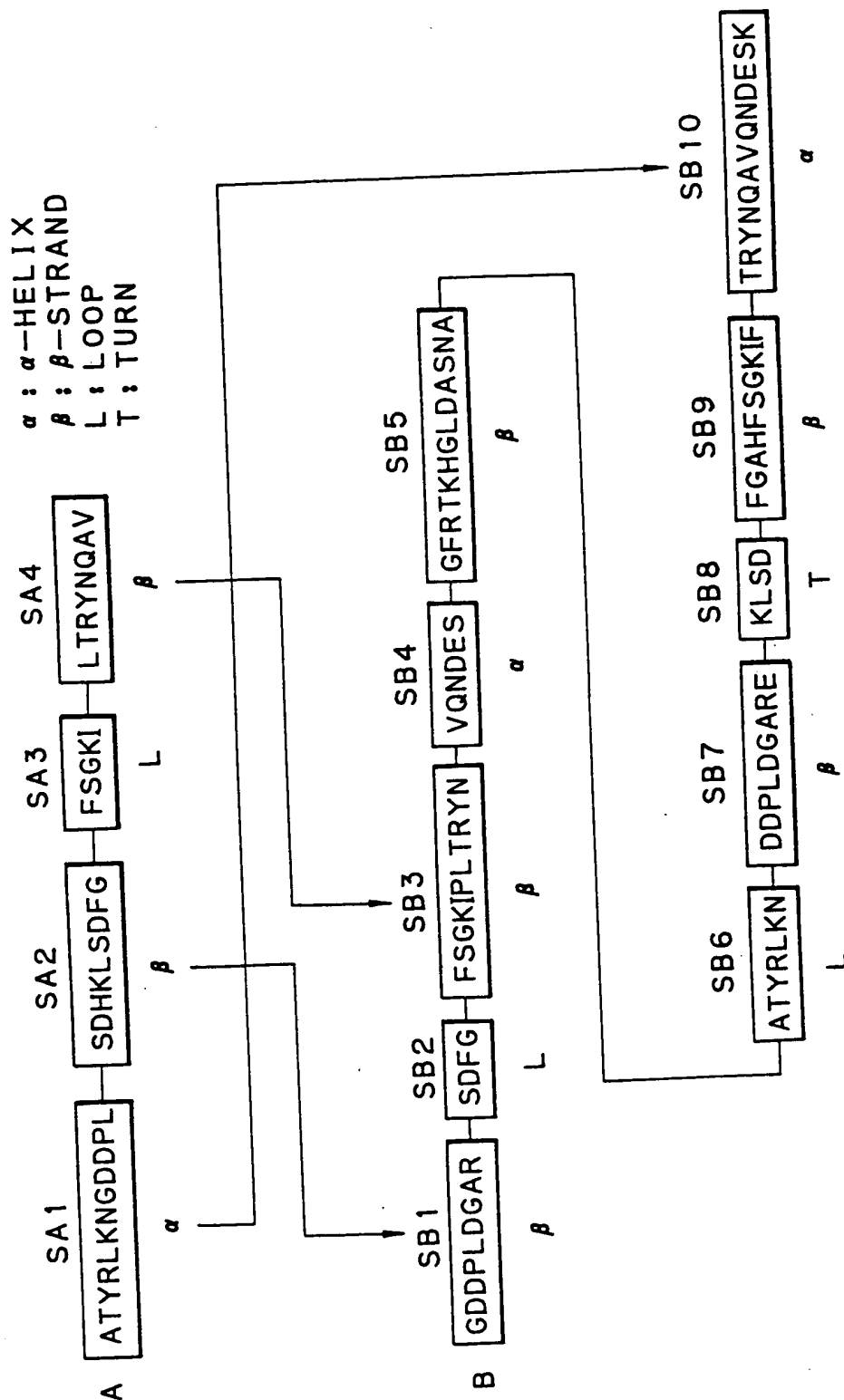
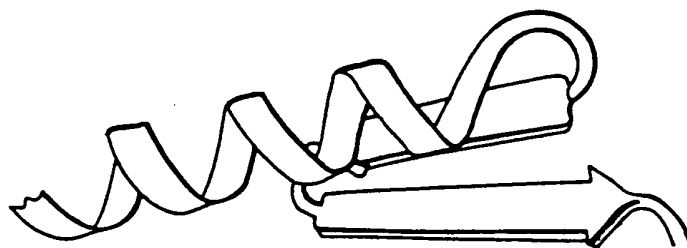
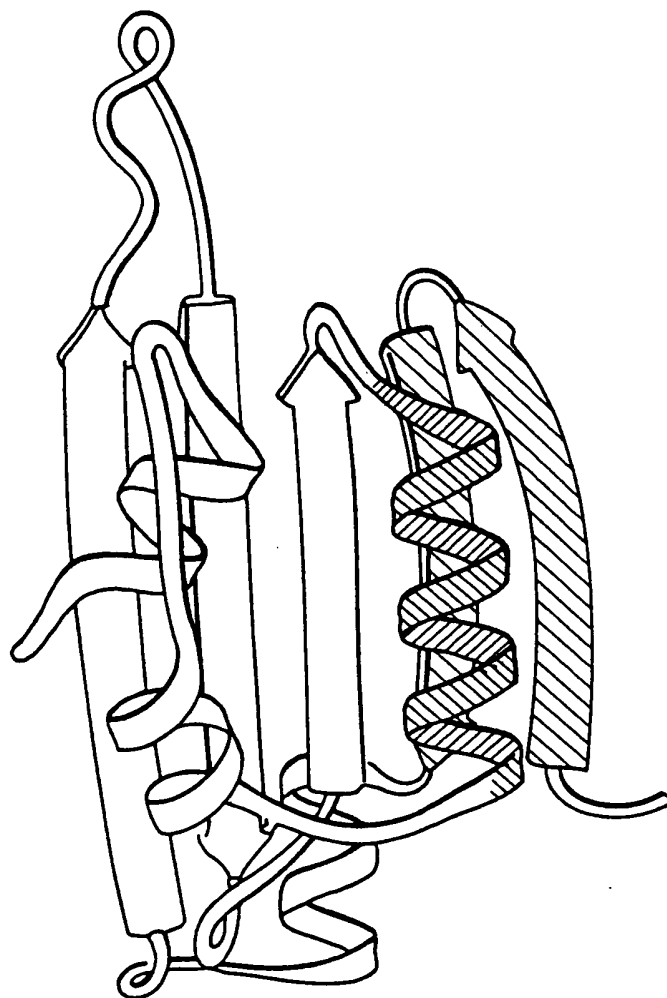


Fig. 47 A



KEY PROTEIN A

Fig. 47 B



PROTEIN B HAVING A SIMILAR STRUCTURE